

Project Report: Delivery of Organic Materials to Planets

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Executive Summary

Background and Purpose

The Evolutionary Genomics Focus Group (EGFG) is an alliance of astrobiologists from eight NAI lead institutions combining expertise in molecular evolutionary analysis (primarily), organic chemistry and biochemistry, Earth history, and paleontology (<http://www.evogenomics.org/>). We use molecular data, especially from sequenced genomes, to illuminate the early history of life and draw comparisons with changes in Earth's environment through time. This work relates to several goals of the NASA Astrobiology Roadmap. The timing of the earliest evolutionary events on Earth is relevant to searches for fossil life on Mars, especially if the early environments of Mars and Earth were similar. The position of organisms occupying extreme environments in the Tree of Life, which is being determined largely through genomic analyses, will help in understanding the influence and importance of those environments (e.g., as found on Europa) on biological evolution. Associations found between the evolution of life on Earth and changes in Earth's environment (e.g., rise in oxygen, a potential biosignature) will have relevance for NASA's Terrestrial Planet Finder (TPF) mission.

Research and Activities

Research and activities in this focus group have involved workshops, videoconferences, direct collaborations, and independent research, all of which have been catalyzed by NAI augmentation support. A balance of independent and team research is desirable, and the success of this alliance (focus group) has been in bringing together researchers with diverse views so they can be heard and discussed. Our research has centered on two areas, (1) phylogeny and timescale, and (2) gene functions and evolution. Highlights of this research are discussed briefly below.

1. Phylogeny and timescale

Several studies involving evolutionary relationships and timing have been completed. They include studies of the earliest splits in life, the Neoproterozoic (time of development of complex life), and comparisons with the fossil record.

Earliest events. Many genes were transferred horizontally during or after the symbiotic events in eukaryote evolution, permitting the timing of those events with molecular clocks. With genomic data, an early split (about 4 billion years

ago, or 4Ga) was estimated for archaeobacteria and the archaeobacterial genes in eukaryotes, and at least two gene-transfer events were identified in the origin of eukaryotes, at 2.7 Ga (premitochondrial) and 1.8 Ga (mitochondrial). Time estimates for the origin of cyanobacteria (2.6 Ga) and the divergence of an early-branching eukaryote that lacks mitochondria (*Giardia*) (2.2 Ga) fall between those two events (Hedges et al., 2001). Those times have implications for early Earth atmosphere (oxygen) and the origin of eukaryotes.

Planetary-scale environmental disturbance. The late Precambrian was a remarkable time in Earth history because of several apparent cycles (750–580 million years ago) of global glaciations (?Snowball Earth events?) followed by the Cambrian explosion of animals. In a recent study, the colonization of land by fungi and plants was timed with many nuclear proteins. (Heckman et al., 2001). The origins of most major lineages were placed deep in the Precambrian, 1.4–0.7 Ga, considerably earlier than their fossils. Because fungi can enhance weathering, which in turn can lead to lower CO₂ levels and global temperatures, and because land plants can bury carbon and generate oxygen, this may explain lower global temperatures and a rise in oxygen in the Neoproterozoic.

The possible relationship between these environmental disturbances and biological evolution, especially complex life (animals), is a major interest of the focus group. (Runnegar, 2000). After one workshop and several videoconferences, a proposal was produced in February detailing the methods and data needed to test several hypotheses (fig. 1).

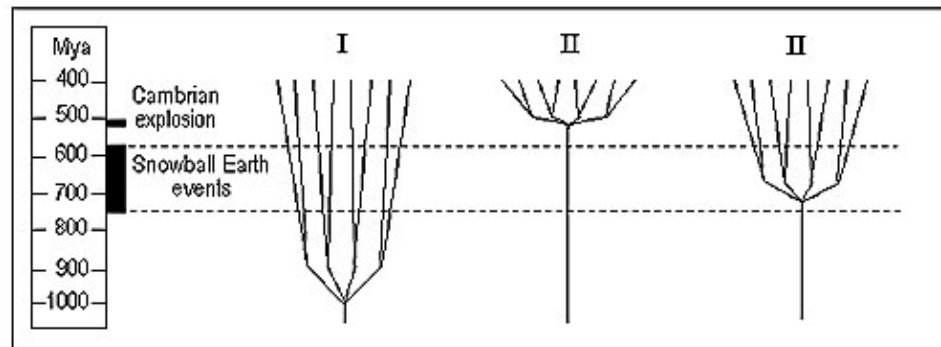


Figure 1. Three possible patterns of animal evolution (divergences of phyla) in relation to global glaciation events of the Precambrian.

Clock calibrations and the fossil record. The discordance between molecular clock dates and fossil-based divergence times is particularly pronounced for the time of origin of the animal phyla, and for the living orders of birds and mammals, including primates. A method for estimating the initial divergence times of clades using an admittedly incomplete fossil record was proposed (Tavare et al., 2002). While Although a literal reading of the fossil record predicts a time of origin of primates some 55 million years ago, the proposed method predicts a time of origin of about 80 million years ago, similar to that estimated by molecular clocks.

1. Gene function and evolution

The biological function of a protein from a living system must be understood in its various contexts: the pathway, the cell, the organism, and ultimately the ecosystem and the biogeosphere. Knowledge of natural history, the fossil record, and geological record can improve our understanding of biomolecular function. Research here includes documentation of recruitment in prokaryotic and eukaryotic proteins and development of computational tools with which to extract signals of form and function. In turn, these data will help to reveal patterns in adaptation at the molecular level that are pertinent to astrobiology. For example, application of these tools to individual protein families has developed our understanding of the planetary biology of digestive proteins in diverse organisms (Benner et al., 2002).

The lateral movement of gene sequences between organisms, as opposed to normal (vertical) evolution, was likely a major factor in the early evolution of genomes, although the full extent of its influence has yet to be determined. Research by several members of the focus group is directed toward a better understanding of such mechanisms of gene evolution. Some of this work has led to the proposal of a new mechanism for codon recognition during protein synthesis (Simonson and Lake, 2002). Comparing distantly related proteins by using an array of bioinformatics tools makes it possible to infer the branching history of genes and superfamilies of genes in order to probe into the earliest stages of protein evolution (Liang Riley, 2001).

References cited (see full list of publications at www.evogenomics.net)

Benner SA, Caraco MD, Thomson JM, Gaucher EA. (2002). Planetary biology – paleontological, geological, and molecular histories of life. *Science*, 296: 864–868.

Heckman DS, Geiser DM, Eidell BL, Stauffer RL, Kardos NL, Hedges SB. (2001). Molecular evidence for the early colonization of land by fungi and plants. *Science*, 293: 1129–1133.

Hedges SB, Chen H, Kumar S, Wang DY–C, Thompson AS, Watanabe H. (2001). A genomic timescale for the origin of eukaryotes. *BMC Evolutionary Biology*, 1: 4.

Liang P, Riley M. (2001). A comparative genomics approach for studying ancestral proteins and evolution. *Advances in Applied Microbiology*, 50: 39–72.

Runnegar B. (2000). Loophole for snowball Earth. *Nature*, 405: 403–404.

Simonson, AB Lake, JA (2002). The Transorientation hypothesis for codon recognition during protein synthesis. *Nature*, 416: 281–285.

Tavare, S, Marshall, CR, Will, O, Soligo, C, Martin, RD. (2002). Estimating the age of the last common ancestor of extant primates using the fossil record. *Nature*, 416: 726–729.

[Focus Group Description & Activities](#)

Three focus group activities took place during Year 4: continuing research and publication, Animal Origins Project proposal, and a focus group breakout session at the Astrobiology Science Conference (NASA Ames Research Center, April).

1. Research progress. Research continued on projects supported by the NAI augmentation funding to some members of the group (Hedges, Lake, Runnegar, Jacobs, Riley, Benner, Marshall). This, and other research by our focus group members led to many publications during Year 4 (see www.evogenomics.net for publication lists by year).
2. Animal origins project. Since the formation of this focus group in 2000, we have had videoconferences, a workshop, and other discussions about a large joint research project involving collection of many DNA sequences (>300,000) from all groups of animals to examine the possible connection between the late Precambrian environment and evolution of complex life (discussed above in *Executive Summary*). These discussions were transformed into a proposal in February entitled "Animal origins project: an evolutionary genomic approach to the study of planetary-scale environmental disturbance." Regardless of the success or failure of the proposal, this activity would not have taken place without the creation of this NAI focus group. Discussions and exchanges that led to the proposal already have enhanced the research of individual focus group members.
3. AbSciCon-2 breakout session. Members of the focus group met during the Second Astrobiology Science Conference at Ames Research Center in April. This occurred informally during the meeting and formally at a breakout session on one of the meeting days. During that session the focus group and NAI focus group pamphlets were distributed for nonmembers in attendance, and the Animal Origins Project was discussed.

Animal Origins Project: The focus group drafted a proposal detailing the methods and data needed to test the hypothesis that planetary disturbances in the late Precambrian (e.g., Snowball Earths) influenced the evolution of complex life.

Planetary biology: Research by members of our focus group was discussed in a review article and placed in the context of planetary biology and understanding the coevolution of Earth and its biota (NASA's Astrobiology Roadmap Goal 2) (*Science* 296:864–868; 3 May 2002; Benner Lab).

Transorientation hypothesis: A new model was proposed for a crucial step in protein synthesis, consistent with the notion of an "RNA World" (*Nature* 416:281–285; 21 March 2002; Lake Lab).

Early colonization of land: It was discovered, with molecular clocks, that fungi and land plants appeared much earlier than predicted by the fossil record, possibly affecting the global environment in the late Precambrian (*Science* 293:1129–1133; 10 August, 2001; Hedges Lab).

Highlights

- A major focus group activity was completed in Year 4 with the drafting of a proposal (Animal Origin's Project) detailing the methods and data needed to test the hypothesis that planetary disturbances in the late Precambrian (e.g., snowball Earths) influenced the evolution of complex life. Also, 15 publications by focus group members appeared in prestigious journals over the last 12 months, including three in *Science*, five in *Nature*, and seven in *PNAS*. Several of these have been discussed above.

Roadmap Objectives

- [**Objective No. 2: Origin of Life's Cellular Components**](#)
- [**Objective No. 3: Models for Life**](#)
- [**Objective No. 4: Genomic Clues to Evolution**](#)
- [**Objective No. 5: Linking Planetary Biological Evolution**](#)
- [**Objective No. 7: Extremes of Life**](#)
- [**Objective No. 8: Past Present Life on Mars**](#)
- [**Objective No. 12: Effects of Climate Geology on Habitability**](#)
- [**Objective No. 13: Extrasolar Biomarkers**](#)
- [**Objective No. 14: Ecosystem Response to Rapid Environmental Change**](#)

Mission Involvement

Mission Class*	Mission Name (for class 1 or 2) OR Concept (for class 3)	Type of Involvement**
2	TPF	background research
3	Europa	background research
3	Mars	background research

* Mission Class: Select 1 of 3 Mission Class types below to classify your project:

1. Now flying OR Funded & in development (e.g., Mars Odyssey, MER 2003, Kepler)
2. Named mission under study / in development, but not yet funded (e.g., TPF, Mars Lander 2009)
3. Long-lead future mission / societal issues (e.g., far-future Mars or Europa, biomarkers, life definition)

** Type of Involvement = Role / Relationship with Mission

Specify one (or more) of the following: PI, Co-I, Science Team member, planning support, data analysis, background research, instrument/payload development, research or analysis techniques, other (specify).

In each of the three cases above, research in the Evolutionary Genomics

Focus Group contributes to the predictive ability of NASA to identify life elsewhere. This is accomplished largely through biomarkers, the interpretation of which is based on the evolution and characteristics of life on Earth. We help to identify and refine these biomarkers by clarifying the relationship between biotic and environmental evolution. An additional, mission-related aspect of this work is the study of the persistence of life (inferred through evolutionary analyses) during environmental extremes in the history of Earth, such as the global glaciations of the Neoproterozoic. In the case of the Terrestrial Planet Finder mission (TPF), the elaboration of historical patterns of early life on Earth and correlations with development of the atmosphere provide an atmospheric biomarker for interpreting spectral analyses. In the case of Mars and Europa, the biomarkers are temporal and environmental (e.g., in drawing comparisons with the history of life on Earth), and any living organisms discovered will require biochemical understanding based on experience with the genetic and genomic complexity of life on Earth.